

*Building the Knowledge Base on  
Genes and Population Health:  
Need for Global Collaboration*

Muin J. Khoury, MD, Ph.D.

**CDC Office of Genomics and Disease Prevention**



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## The case for a global human genome epidemiology initiative

**To the editor:**  
Collins argues for a large population-based prospective cohort study in the US to assess the role of genes and environment in common diseases<sup>1</sup>. Without such a study, he

genes contribute a substantial population attributable fraction. Even if variation at each locus can be classified dichotomously (susceptible versus nonsusceptible genotype), this will create  $2^{10}$  (>1,000)

scheme of newly diagnosed cases in well-defined communities and appropriately selected controls. Well-designed population-based incident case-control studies can even be nested in a larger population cohort or

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**Khoury MJ, Nat Genet 2004;36:1027-8**



## *Outline: Three Messages*

- ✍ Global Collaboration in Biobanks/Population-based Cohort Studies
  - ✍ One cohort study in one country is not enough!
- ✍ Integration of all Human Genome Epidemiologic Data (cohort, case-control, other)
  - ✍ There is more than one way to get there!
- ✍ Development of Evidence-based Processes that use Human Genome Epidemiologic Data
  - ✍ Direct link from epidemiology to practice!

# *The Epidemiologic Approach to Genes and Health in Populations: Human Genome Epidemiology (HuGE)*

- ✍ **Gene Discovery:** Mostly from family Studies, LD mapping usually from convenient, non-representative groups
- ✍ **Population-based epidemiologic studies:**
  - ✍ Gene Variant Characterization: prevalence, gene-disease associations in terms of relative, absolute and attributable risks
  - ✍ Gene Variant Characterization: gene-gene and gene-environment interaction

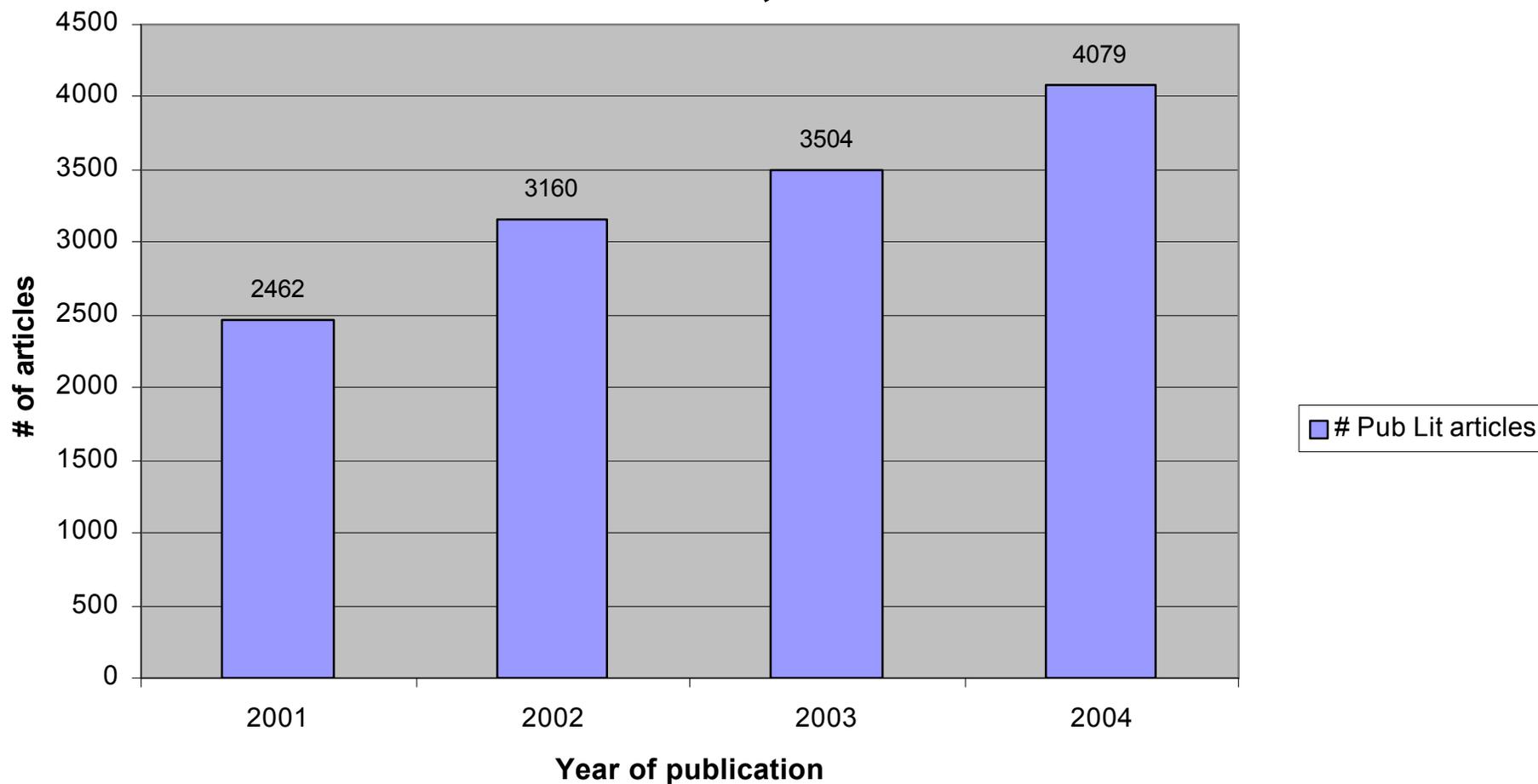
# *Types of Epidemiologic Studies for Gene Characterization in Populations*

- ✍ Cross sectional studies
- ✍ Case-control studies
- ✍ Cohort studies
- ✍ Population biobanks

## ✍ **Myths:**

- ✍ **Stigma around “association studies”**
- ✍ **Cohort inherently superior to case-control studies**

# No. of articles in Huge Published Literature db, 2001-2004\*



(\*As of Jan 14, 2005. Count excludes review articles, meta & pooled analyses.)

# Number of Published HuGE Papers\* 2001-2004

Year	Prevalence	Associations	Interactions
2001	308	2141	436
2002	349	2799	569
2003	323	3010	598
2004	368	3486	604

•MOST ASSOCIATION STUDIES ARE CASE-CONTROL STUDIES

# NHANES III DNA BANK

## Prevalence of Genes of Public Health Significance

### Background

#### NHANES III DNA Bank

- National Health and Nutrition Examination Survey (NHANES) is a nationally representative survey
- Detailed interviews, clinical, laboratory and radiologic examinations are conducted
- Phenotypic data, such as serostatus for many infectious exposures, blood count, chemistries, etc. were collected
- During second phase NHANES III (1991-1994), white blood cells were frozen and cell lines were immortalized with EBV
- NHANES III DNA bank is located at NCEH/CDC, with specimens available from over 7000 participants
- In 2002, NCHS announced a call for proposals to use these specimens in the Federal Register

### Collaborative CDC-wide Proposal Objective

- Determine the prevalence of genotypes of public health importance



### Criteria for Genetic Variants

#### Public Health Importance

- Known or hypothesized association with diseases of public health importance
- Role in pathways affecting multiple diseases
- Identified functional variants
- Relatively common (i.e., >2.0%)
- Previously described gene-environment or gene-gene interactions
- Relevant phenotypic data available in NHANES dataset
- No current use for clinical risk assessment or intervention

### Challenges to Identifying Genes of Public Health Importance

- Gaps in information in the literature
- Methodological issues of many available studies
  - Selection bias, power, interaction
- Non-registration of gene-disease association



### Public Health Significance of Proposal

- Prevalence of gene variants
  - Basis for estimating population attributable fraction in combination with measure of gene-disease association
  - Enable assessment of potential for screening population subgroups for susceptibility genes
  - Prevalence of combinations of variants in pathways and/or different loci
- Examine gene-disease association, gene-environment and gene-gene interactions

### Selected Pathways of Gene Variants (87 variants of 57 genes)

- Nutrient Metabolism (e.g., folate and homocysteine, lipids, glucose, alcohol, vitamin D)
- Immune and Inflammatory responses (e.g., cytokines, receptors)
- Activation and detoxification pathways (e.g., drugs, carcinogens, environmental contaminants)
- DNA repair pathways (e.g., oxidative variation, environmental toxins)
- Hemostasis pathway and hemostaticism (e.g., vascular) pathway
- Developmental (e.g., hearing loss)

### Laboratory Methods

- Genotyping
  - Assessing Feasibility of External Laboratories to conduct high throughput, accurate, low cost, genotyping for ~600,000 SNPs (~700 specimens x 87 variants)

\*None of gene variants within gene region



### Next Steps

- Pending approval from NCHS
- Laboratory selection
- Genotype-Phenotype analyses

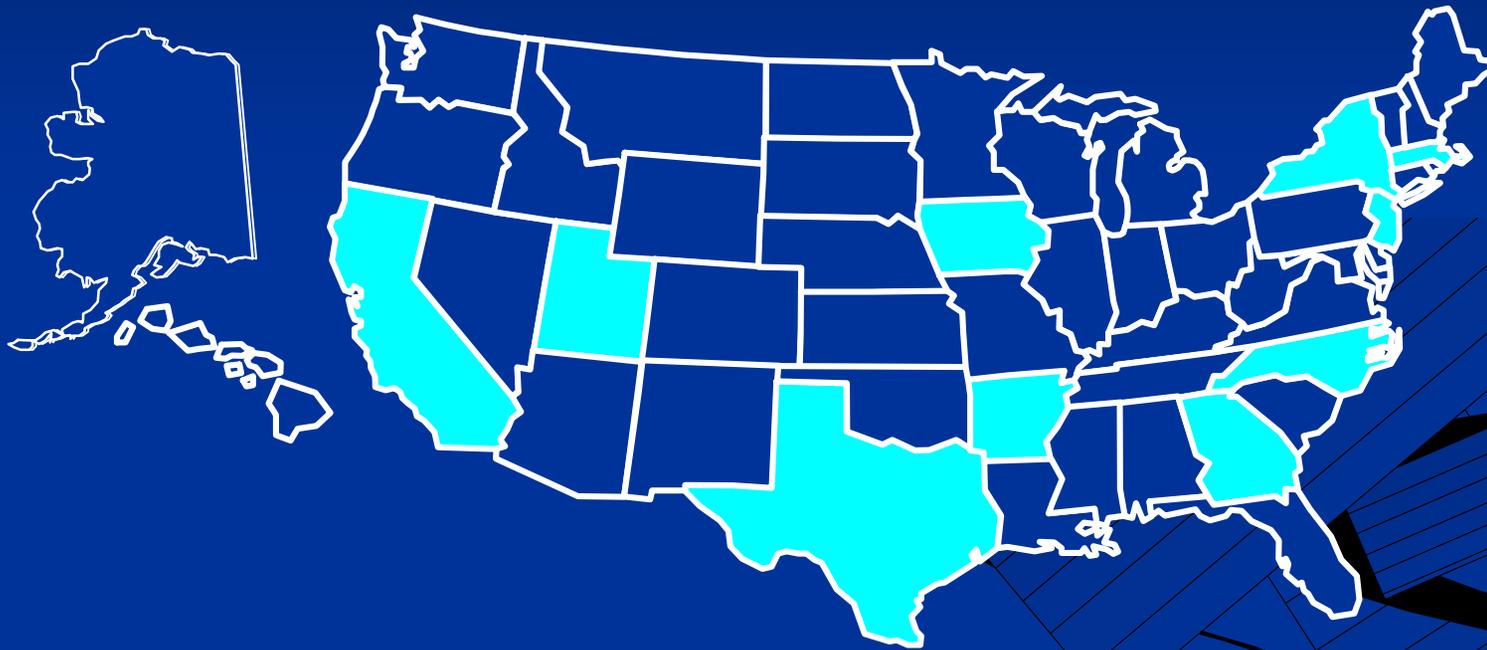
### CDC Working Group

ATSDR: Olivia Harris, NCBDDO: Karen Abe, Cynthia Moore, Lorenza Bobb, Quanhe Yang, NCHSTP: Mary Reichler, NCID: Tom Hodge, Craig Hooper, Jai Lingappa, Janet McNeill, Anne Dille, NCEH: Amanda Brown, Peg Gallagher, Maria Gwini, Omar Henderson, Bruce Liu, Mary Lou Lindgren, Julian Little, Karen Steinberg, NCCDPHP: Heidi Blanco, Wayne Glass, Ingrid Hall, Giuseppina Imperatore, Ann Malencher, NIOSH: MaryAnn Butler, Ainsley Weston, PHPPO: Bin Chen, NIP: Scott Campbell, NCHS: Gerry McQuillen



# Centers for Birth Defects Research and Prevention

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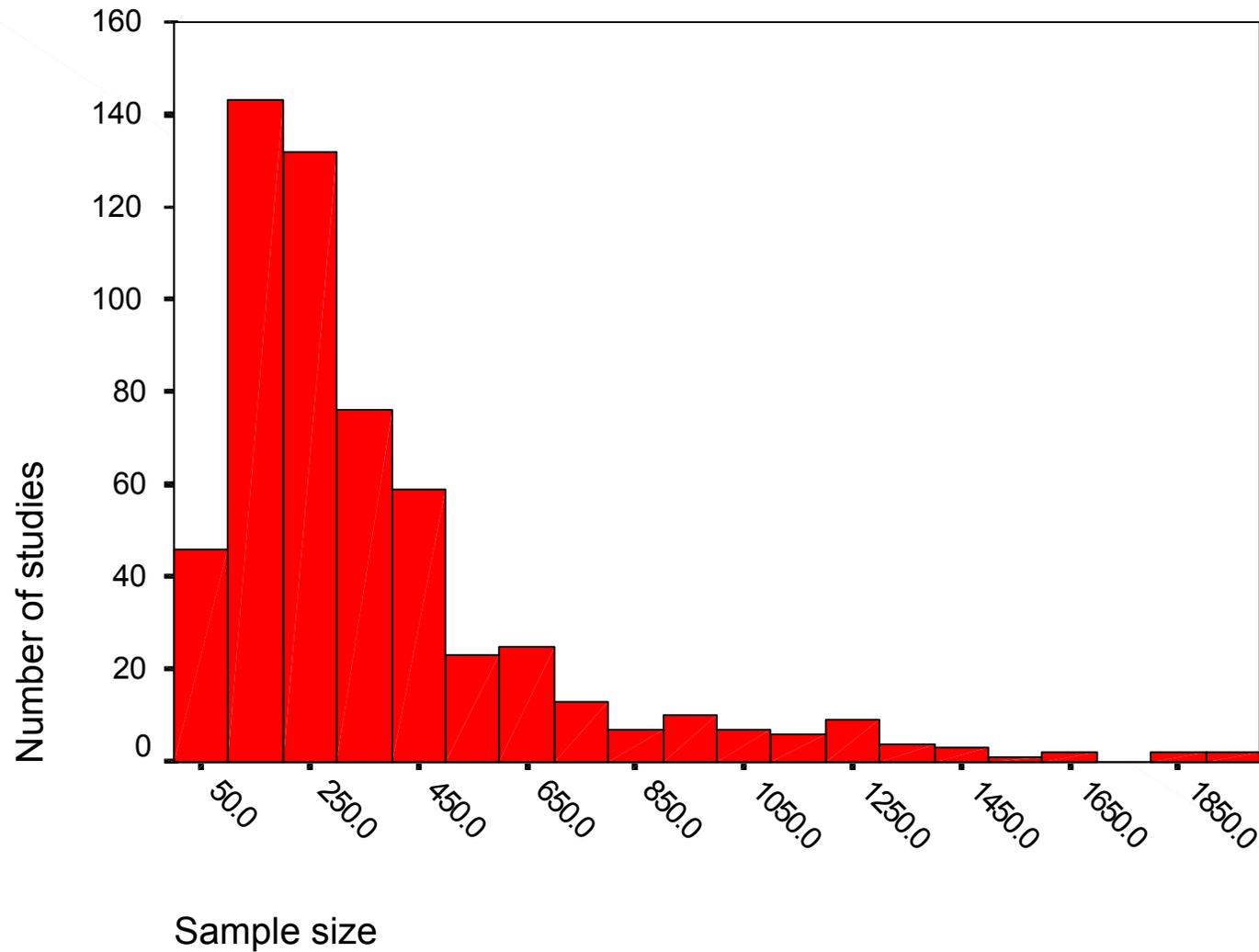


**Multi-state Population-Based Case-Control Study  
Based on State-Based Birth Defects Registries**

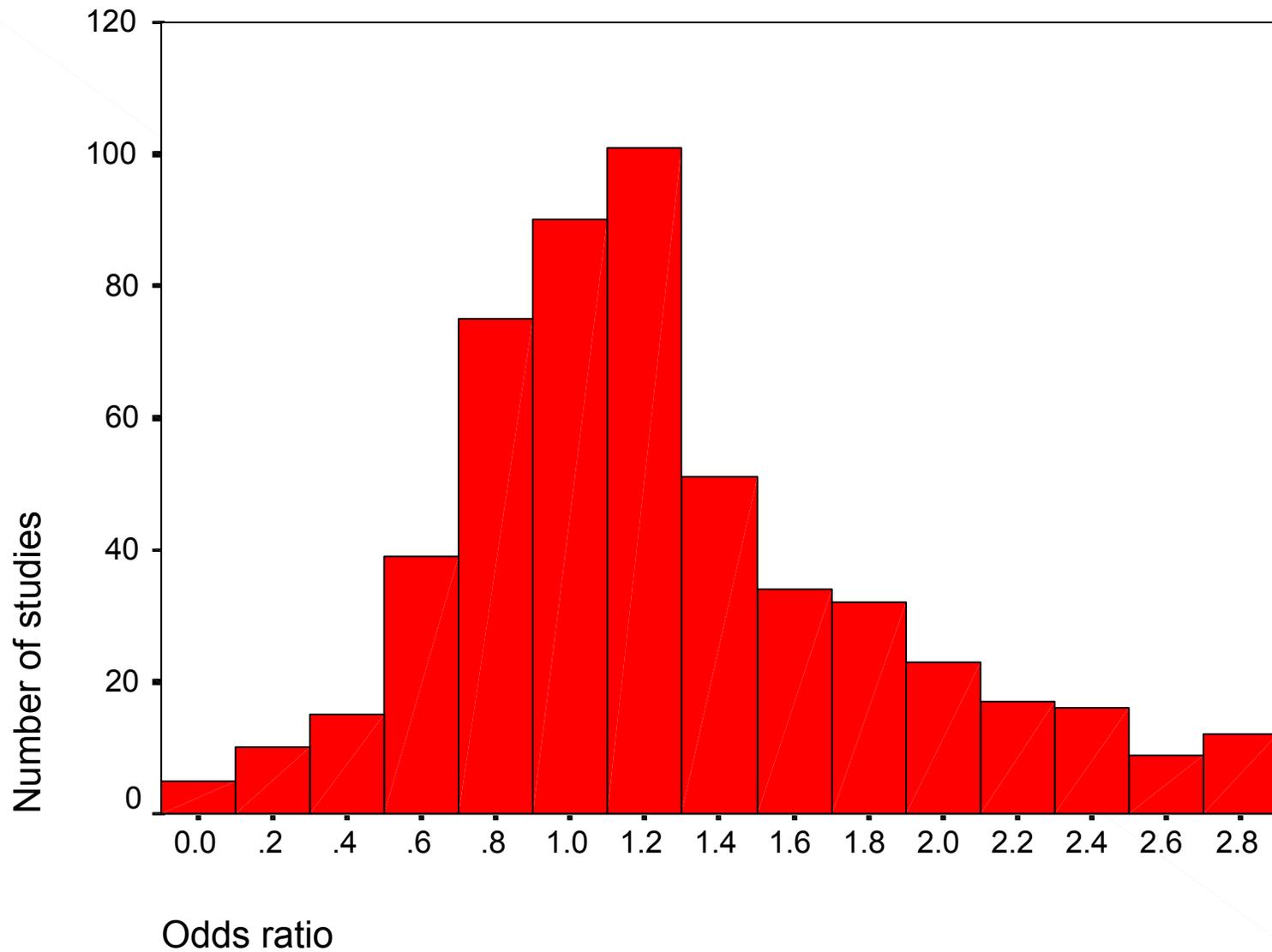
# *The Need for Integrating Epidemiologic Evidence: on Genes and Population Health*

- ✍ Unmanageable amounts of data
- ✍ Small sample size of individual studies
- ✍ Small effect size of gene-disease associations
- ✍ Replication of associations
- ✍ Publication bias
- ✍ Heterogeneity
- ✍ Generate and test hypotheses

## *Small sample size of individual studies*



## *Small effect sizes in individual studies*



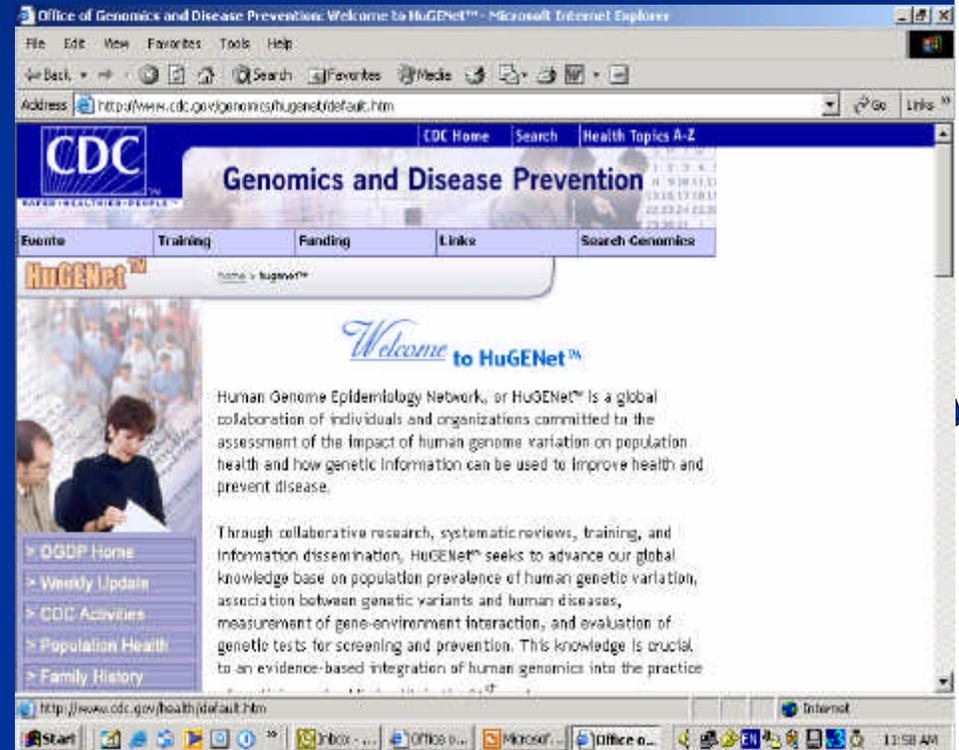
## *How to Build the Knowledge Base on Genes and Population Health*

- ✍ Single large population cohort study
- ✍ Systematic synthesis of data from existing and planned cohort studies
- ✍ Systematic synthesis of data from all epidemiologic studies (cohorts, case-control, etc)
- ✍ Accelerated systematic synthesis of group and individual data using collaborative networks and consortia of all types of studies (cohorts, case-control, etc)
- ✍ All of the above

# Human Genome Epidemiology Network (HuGE Net)

✍ Global collaboration of individuals and organizations to assess population impact of genomics and how it can be used to improve health and prevent disease

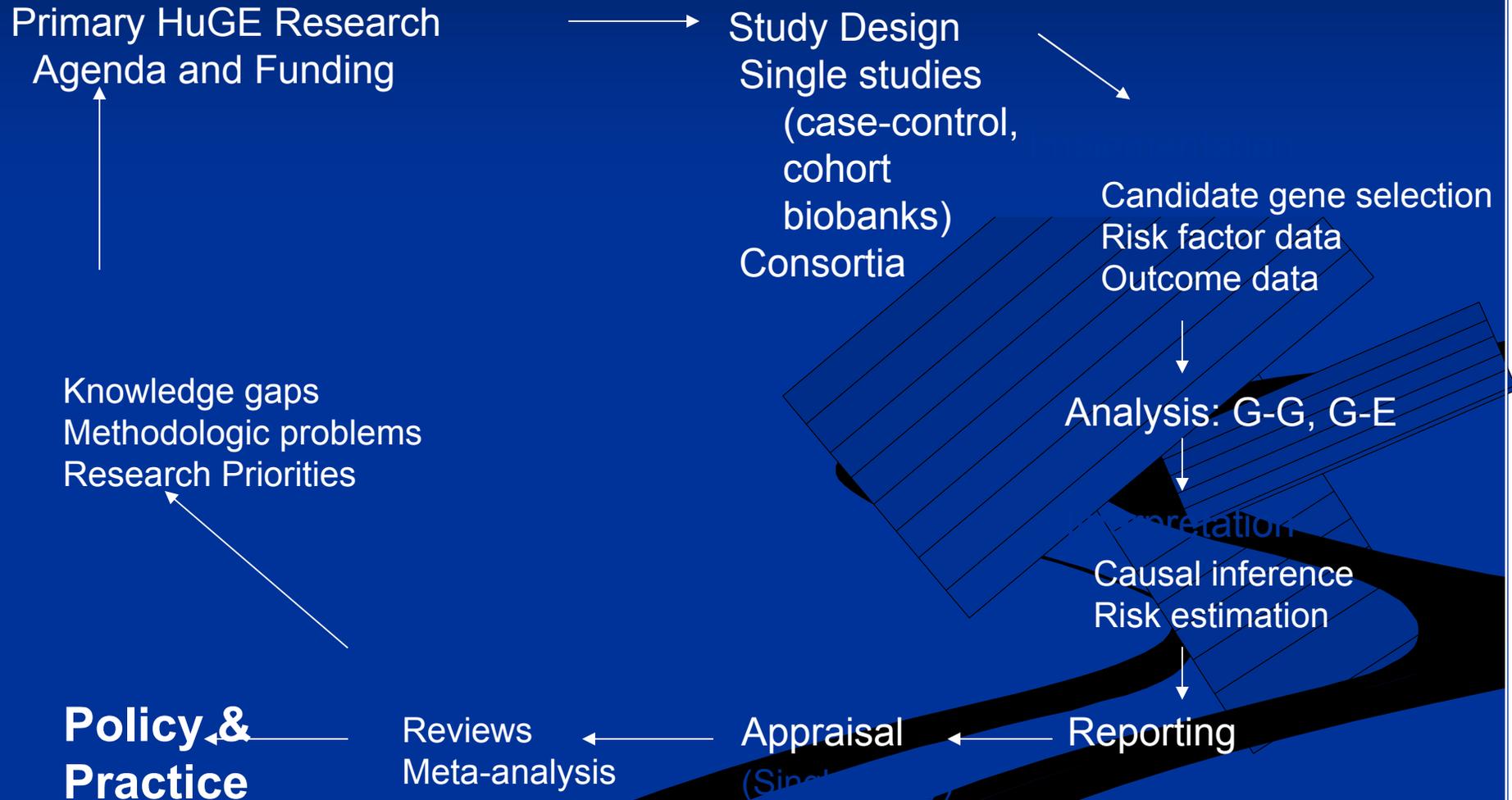
- ✍ Information Exchange
- ✍ Training and Technical Assistance
- ✍ Knowledge Base Development
- ✍ Information Dissemination



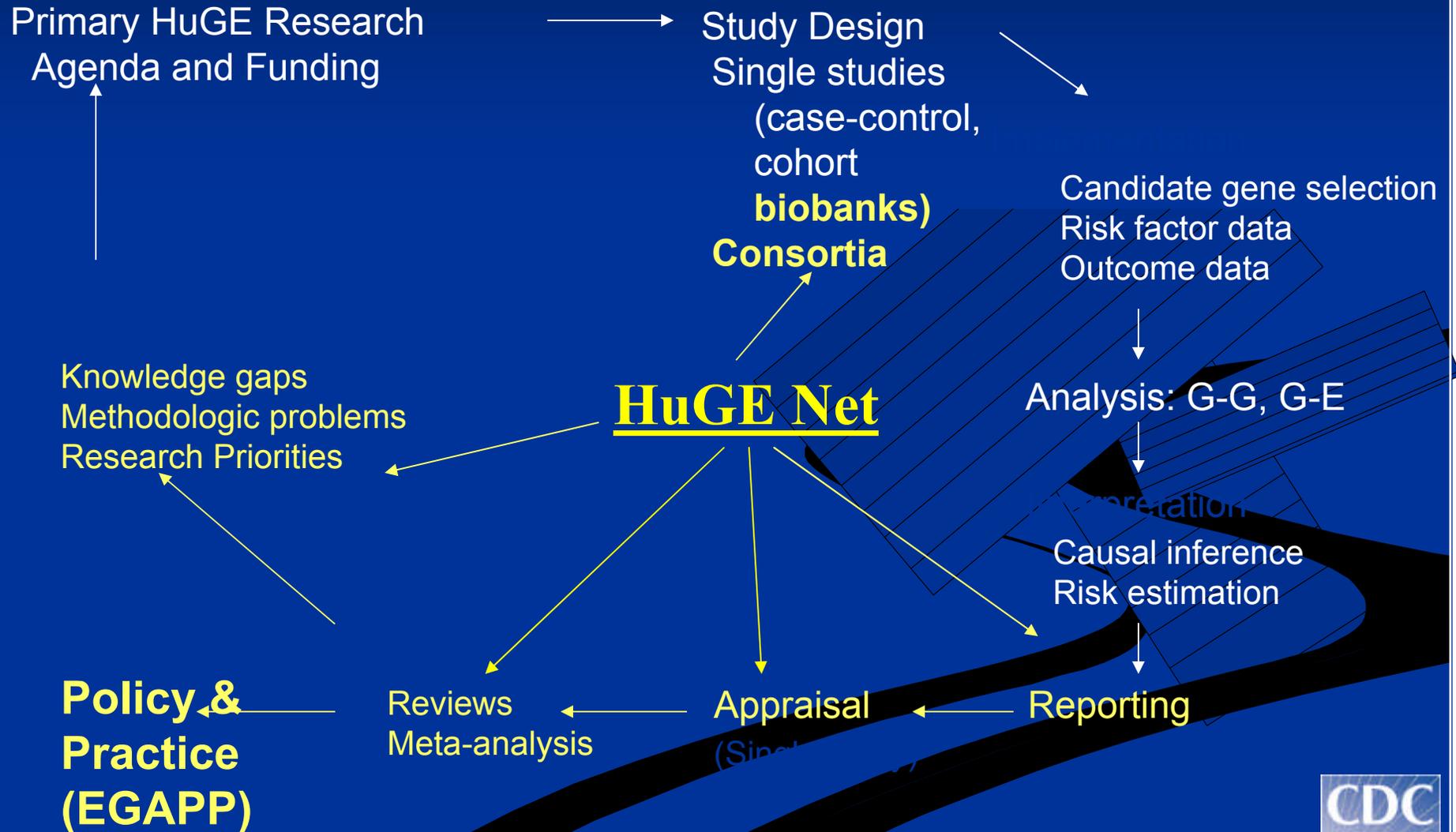
# *Selected HuGE Net Activities*

- ✍ HuGE Studies Database
- ✍ HuGE Reviews
- ✍ Methodology/Training Workshops
- ✍ International Biobank/Cohort Study meeting
- ✍ “Network of Networks”
- ✍ Connecting epidemiologic information to evidence-based evaluation of genomic applications in practice and prevention (EGAPP)

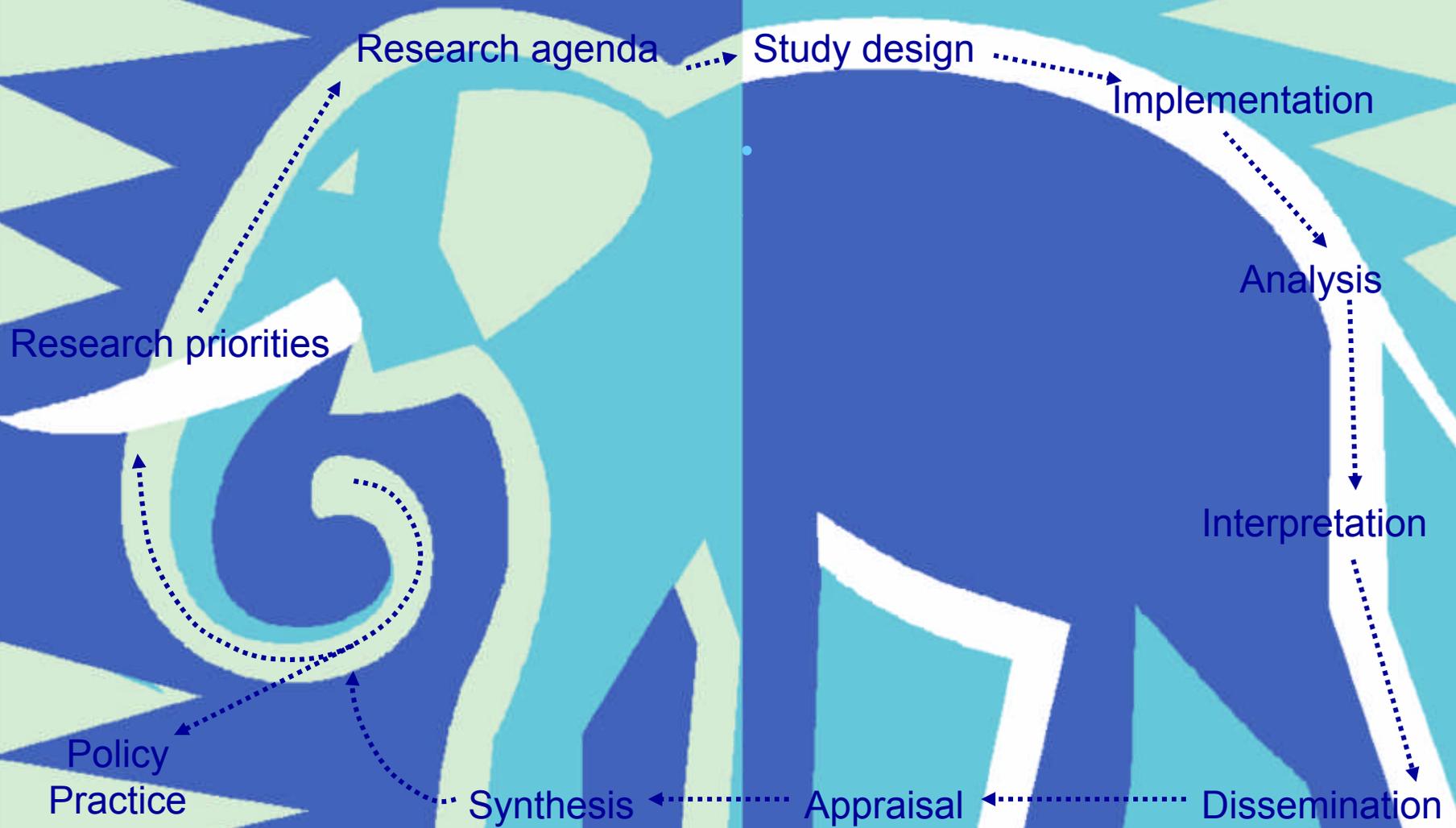
# From HuGE Research to Synthesis & Dissemination for Policy and Practice



# From HuGE Research to Synthesis & Dissemination for Policy and Practice



# The Human Genome Epidemiology Network



# International Biobank and Cohort Studies: Developing a Harmonious Approach



**Sheridan Buckhead Hotel**  
**Atlanta, GA**  
**February 7-8, 2005**



# ***Biobank Meeting Discussions and Outcomes***

- ✍ STROBE like statement for publishing studies derived from biobanks
- ✍ General report on the design and conduct of biobanks
- ✍ Online knowledge base with register of studies and tools (e.g. protocols, informed consent)
- ✍ Future periodic meetings with information sharing

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